

A3 9. (Amended) The method of claim 1, wherein said tandem repeats encode at least one sequence selected from the group consisting of LKPNM (SEQ ID NO:1), KPNM (SEQ ID NO:2), VVYP (SEQ ID NO:3), KPN, DKP, YKP, EKP, DAP, EAP, HPP, VPP, LK, PN and NM.

REMARKS

Applicants have amended the specification to refer to SEQ ID NOs. for amino acid sequences of four or more amino acids. All amino acid sequences of at least four amino acids are now included in the Sequence Listing in compliance with 37 C.F.R. § 1.821. The Sequence Listing and computer readable form (CRF) copy are in compliance with the requirements of 37 C.F.R. 1.821-1.825 and a substitute paper copy of the Sequence Listing and CRF copy and a Statement As Required Under 37 C.F.R. § 1.825(a) and (b) Statement As Required Under 37 C.F.R. § 1.821(g) are submitted herewith.

No new matter is introduced by this amendment. Should the Examiner have any questions or comments regarding this matter, a telephone call to the undersigned Applicants' representative is earnestly solicited.

REQUEST FOR EXTENSION OF TIME

Pursuant to 37 C.F.R. § 1.136(a), Applicants petition for an extension of time of one month to and including November 30, 2002, in which to respond to the Office Communication dated October 1, 2002. Pursuant to 37 C.F.R. § 1.17, a check in the amount of \$110.00 is enclosed, which is the process fee for a one-month extension of time.

If the check is inadvertently omitted, or should any additional fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to the enclosed materials, or should an overpayment be included herein, the Commissioner is authorized to deduct or credit said fees from or to Fulbright & Jaworski Deposit Account No. 50-1212/MONS:016US.

Respectfully submitted,



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APPENDIX A
MARKED VERSION TO SHOW CHANGES

In The Specification

Please replace the paragraphs beginning on page 6, line 36 and ending on page 7, line 28, with the following rewritten paragraphs:

Still another aspect of the invention, provides a polynucleotide of the formula $A_w [L_x S_n]_y B_z$ and its complement where, A is a nucleotide sequence containing at least one restriction enzyme site; L is a nucleotide sequence containing at least one chemical or enzymatic cleavage site; S is a degenerate nucleotide sequence encoding one of the amino acid sequences selected from the group consisting of LKPNM (SEQ ID NO:1), KPNM (SEQ ID NO:2), VVYP (SEQ ID NO:3), KPN, DKP, YKP EKP, DAP, EAP, HPP, VPP, LK, PN and NM such that S's with different values of n comprise different nucleotide sequences, but encode the same amino acid sequence; B is a nucleotide sequence containing at least one restriction enzyme site, where B may or may not be the same as A; w is 0 or 1; x is 0 or 1; n varies randomly with each S, and is a whole number from 1 to the maximum number of possible nucleotide sequences encoding the amino acid sequence of S; y is at least 2; and z is 0 or 1.

In another aspect of the invention, is provided a polynucleotide of the formula $A_w [L_x S_n T_m]_y B_z$ and its complement where, A is a nucleotide sequence containing at least one restriction enzyme site; L is a nucleotide sequence containing at least one chemical or enzymatic cleavage site; S is a degenerate nucleotide sequence encoding one of the amino acid sequences selected from the group consisting of LKPNM (SEQ ID NO:1), KPNM (SEQ ID NO:2), VVYP (SEQ ID NO:3), KPN, DKP, YKP EKP, DAP, EAP, HPP, VPP, LK, PN and NM such that S's with different values of n comprise different nucleotide sequences, but encode the same amino acid sequence; T is a degenerate nucleotide sequence encoding one of the amino acid sequences selected from the group consisting of LKPNM (SEQ ID NO:1), KPNM (SEQ ID NO:2), VVYP (SEQ ID NO:3), KPN, DKP, YKP EKP, DAP, EAP, HPP, VPP, LK, PN and NM such that the sequence of T encodes an amino acid sequence different from S, and T's with different values of m comprise different nucleotide sequences, but encode the same amino acid sequence; B is a nucleotide sequence containing at least one restriction enzyme site, where B may or may not be the same as A; w is 0 or 1; x is 0 or 1; n varies randomly with each S, and is a whole number from 1 to the maximum number of possible nucleotide sequences encoding the amino acid sequence of S; m varies randomly with each T, and is a whole number from 1 to the maximum number of possible nucleotide sequences encoding the amino acid sequence of T; y is at least 2; and z is 0 or 1.